

WEST Search History

[Hide Items](#)[Restore](#)[Clear](#)[Cancel](#)

DATE: Monday, November 07, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
		<i>DB=USPT,PGPB; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L16	("ISH-HOROWICZ-DAVID".IN.)!	7
		<i>DB=PGPB,USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L15	l14 and @ay<1999	17
<input type="checkbox"/>	L14	L13 and l11	113
<input type="checkbox"/>	L13	delta\$2 adj8 antibod\$4	524
<input type="checkbox"/>	L12	delta\$2 8adj antibod\$4	0
<input type="checkbox"/>	L11	L10 and antibod\$	5458
<input type="checkbox"/>	L10	L9 and (bertebrate or mammal\$3 or human)	6202
<input type="checkbox"/>	L9	L6 and ((tyrosine kinase) or jagged or dsl)	6282
<input type="checkbox"/>	L8	L7 and antibod\$	16279
<input type="checkbox"/>	L7	L6 and (vertebrate or mammal\$3 or human)	20893
<input type="checkbox"/>	L6	Delta\$2 and (notch or kinase)	28615
<input type="checkbox"/>	L5	Delta and (notch or kinase)	24202
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	6121045.pn.	1
<input type="checkbox"/>	L3	6337387.pn.	1
<input type="checkbox"/>	L2	6262025.pn.	1
<input type="checkbox"/>	L1	5834208.pn.	1

END OF SEARCH HISTORY

(FILE 'HOME' ENTERED AT 13:00:13 ON 07 NOV 2005)

FILE 'MEDLINE' ENTERED AT 13:00:28 ON 07 NOV 2005
E SAKANO S/AU

L1 60 S E3-E4
L2 9 S L1 AND KINASE

FILE 'STNGUIDE' ENTERED AT 13:01:56 ON 07 NOV 2005

FILE 'GENBANK' ENTERED AT 13:02:40 ON 07 NOV 2005
SET NOTICE DISPLAY 1
SET NOTICE LOGIN DISPLAY

FILE 'MEDLINE' ENTERED AT 13:04:09 ON 07 NOV 2005

=>

STIC-Biotech/ChemLib

170868

From: Chan, Christina
Sent: Monday, November 07, 2005 2:55 PM
To: Kaufman, Claire; STIC-Biotech/ChemLib
Subject: RE: rush sequence search 09/783931

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
NOV - 7 2005
STIC-BIOTECH/CHM LIB
(STIC)

-----Original Message-----

From: Kaufman, Claire
Sent: Monday, November 07, 2005 12:24 PM
To: Chan, Christina
Subject: FW: rush sequence search 09/783931

Christina, I need a rush sequence search for a due an after final that is allowable. Please forward this request to STIC. Thanks, Claire

RUSH ***** RUSH ***** RUSH ***** RUSH*****

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX:Rem 4C70
Room:Rem 4E85 Serial #:09/783,931 Date:11/07/05

Please search nucleic acid sequences SEQ ID NO:24 in interference databases only.

Please show top 30 hits.

Please put results on disk.

Thanks,
Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

4C70

Searcher: am
Searcher Phone: 22504
Date Searcher Picked up: 11/8
Date completed: 11/14
Searcher Prep Time: 10
Online Time: 26

Type of Search
NA# ✓ AA#
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: ✓
WWW/Internet:
Other (Specify):

From: Kaufman, Claire
Sent: Thursday, July 14, 2005 12:21 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/783931

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70
Room: Rem 4E85 Serial #: 09/783931 Date: 7/14/05

Please search SEQ ID NO:23 in commercial databases.

Please put results on disk.

Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

STIC-Biotech/ChemLib

158956

From: Kaufman, Claire
Sent: Tuesday, July 12, 2005 9:29 AM
To: STIC-Biotech/ChemLib
Subject: FW: rush sequence search 09/783931

-----Original Message-----

From: Low, Christopher
Sent: Monday, July 11, 2005 4:53 PM
To: Kaufman, Claire
Subject: RE: rush sequence search 09/783931

approved

Christopher Low
SPE 1614 / TCAR 1600
REM 3E88 / (571) 272-0951

-----Original Message-----

From: Kaufman, Claire
Sent: Monday, July 11, 2005 02:51 PM
To: Low, Christopher
Subject: rush sequence search 09/783931

Chris, I need a rush sequence search for a due amended that is allowable (much to my surprise). Please forward this request to STIC. Thanks, Claire

RUSH ***** RUSH ***** RUSH ***** RUSH***

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70
Room: Rem 4E85 Serial #: 09/783,931 Date: 7/11/05

Please search nucleic acid sequences SEQ ID NO: 1, 11, 14 and 26
and protein sequences SEQ ID NO: 2, 12 and 65 in interference databases only.

For nucleic acid sequences, please list top 30 hits.

Please put results on disk.

Thanks,
Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

STAFF USE ONLY

Searcher: D. Schreyber
Searcher Phone: 2- 2526
Date Searcher Picked up: 7/18
Date Completed: 7/18
Searcher Prep/Rev. Time: 23
Online Time: 8

Type of Search

NA#: 4 AA#: 3
Interference: / SPDI:
S/L: Oligomer:
Encode/Transl:
Structure#: Text:
Inventor: Litigation:

Vendors and cost where applicable

STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: Comp 454
WWW/Internet:
Other(Specify):

STIC-Biotech/ChemLib

138232

mej

From: Kaufman, Claire
Sent: Thursday, November 18, 2004 1:57 PM
To: STIC-Biotech/ChemLib
Subject: sequence 09/783,931

RECEIVED
NOV 18 2004
TECH/BIOT. DIVISION
(STIC)

SEQUENCE SEARCH REQUEST

Examiner: Claire Kaufman AU: 1646 MAILBOX: Rem 4C70
Room: Rem 4E85 Serial #: 09/783,931 Date: 11/18/04

Please search SEQ ID NO:65 and the fragment of SEQ ID NO:26 from 60-665 in interference databases only.

Please put results on paper.

Claire Kaufman, AU 1646
Rem 4E85 (571) 272-0873

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

OM nucleic - nucleic search, using sw model

Run on: November 14, 2005, 05:15:01 ; Search time 490 Seconds
(without alignments)
9680.747 Million cell updates/sec

Title: US-09-783-931B-24
Perfect score: 2899
Sequence: 1 gtccagcgggtaccatgggcc.....aataaatataatgaactaca 2899

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2742.8	94.6	2899	3	US-08-981-392-24	Sequence 24, Appl
2	2742.8	94.6	2899	4	US-09-908-322-24	Sequence 24, Appl
3	2371.2	81.8	2857	3	US-08-981-392-4	Sequence 4, Appli
4	2371.2	81.8	2857	4	US-09-908-322-4	Sequence 4, Appli
5	2133.4	73.6	2692	3	US-08-981-392-11	Sequence 11, Appl
6	2133.4	73.6	2692	4	US-09-908-322-11	Sequence 11, Appl
7	1780	61.4	1981	3	US-08-981-392-26	Sequence 26, Appl
8	1780	61.4	1981			

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OM nucleic - nucleic search, using sw model

Run on: November 14, 2005, 05:24:01 ; Search time 2032 Seconds
(without alignments)
11798.330 Million cell updates/sec

Title: US-09-783-931B-24
Perfect score: 2899
Sequence: 1 gtccagcgggtaccatgggcc.....aataaatataatgaactaca 2899

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
- 25: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2742.8	94.6	2899	9	US-09-908-322-24	Sequence 24, Appl	
2	2742.8	94.6	2899	10	US-09-783-931-24	Sequence 24, Appl	
3	2409.6	83.1	2857	20	US-10-731-741-9	Sequence 9, Appli	
4	2409.6	83.1	2857				

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 410.08 Seconds
(without alignments)
10007.261 Million cell updates/sec

Title: US-09-783-931A-1
Perfect score: 2508
Sequence: 1 gaattcggcagcagaggtttt.....tcgataccggtcatcaagctt 2508

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	2508	100.0	2508	3	US-08-981-392-1	Sequence 1, Appli
2	2508	100.0	2508	4	US-09-908-322-1	Sequence 1, Appli
3	2460.6	98.1	2883	3	US-08-981-392-3	Sequence 3, Appli
4	2460.6	98.1	2883	4	US-09-908-322-3	Sequence 3, Appli
5	1442.4	57.5	2663	3	US-09-068-740A-8	Sequence 8, Appli
6	1442.4	57.5	2663	4	US	

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 1545.61 Seconds
(without alignments)
10210.150 Million cell updates/sec

Title: US-09-783-931A-1
Perfect score: 2508
Sequence: 1 gaattcggcagcagaggttttt.....tcgataccggtcatcaagctt 2508

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2508	100.0	2508	9	US-09-908-322-1		Sequence 1, Appli
2	2508	100.0	2508	10	US-09-783-931-1		Sequence 1, Appli
3	2460.6	98.1	2883	9	US-09-908-322-3		Sequence 3, Appli
4	2460.6	98.1	2883	10	US-09-783-931-3		Sequence 3, Appli
5	2458.6	98.0	2883	20	US-10-877-563-10		Sequence 10, Appl
6	1891.8	75.4	2088	20	US-10-877-563-9		Sequence 9, Appli
7	1442.4	57.5					

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:13:45 ; Search time 9833.79 Seconds
(without alignments)
10411.464 Million cell updates/sec

Title: US-09-783-931A-1
Perfect score: 2508
Sequence: 1 gaattcggcagcagaggtttt.....tcgataccggtcatcaagctt 2508

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
4: /cgn2_ /1/pna/US6058_COMB.seq:*
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	2508	100.0	2508	34	US-09-783-931-1	Sequence 1, Appli	
2	2460.6	98.1	2883	34	US-09-783-931-3	Sequence 3, Appli	
3	2458.6	98.0	2883	20	US-09-310-685-10	Sequence 10, Appl	
4	2458.6	98.0	2883	64	US-10-877-563-10	Sequence 10, Appl	
5	2458.6	98.0	2883	68	US-11-022-478-10	Sequence 10, Appl	
6	1891.8	75.4	2088	20	US-09-310-685-9	Sequence 9, Appli	
7	1891.8	75.4	2088	64	US-10-877-563-9	Sequence 9, Appli	
8	1891.8	75.4					

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

```
Run on:      July 14, 2005, 13:02:24 ; Search time 440.166 Seconds
              (without alignments)
              10007.261 Million cell updates/sec
```

Title: US-09-783-931A-11
Perfect score: 2692
Sequence: 1 ctgcaggaattcsmycgcat.....gctcccaacgcgttggaggt 2692

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_NA:*
1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2690.8	100.0	2692	3	US-08-981-392-11	Sequence 11, Appl
2	2690.8	100.0	2692	4	US-09-908-322-11	Sequence 11, Appl
3	2506.6	93.1	2857	3	US-08-981-392-4	Sequence 4, Appli
4	2506.6	93.1	2857	4	US-09-908-322-4	Sequence 4, Appli
5	2133.4	79.2	2899	3	US-08-981-392-24	Sequence 24, Appl
6	2133.4	79.2	2899	4	US-09-908-322-24	Sequence 24, Appl
7	1679.8	62.4	2663	3	US-09-	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

```
Run on:      July 14, 2005, 18:14:14 ; Search time 1659.01 Seconds
              (without alignments)
              10210.150 Million cell updates/sec
```

Title: US-09-783-931A-11
Perfect score: 2692
Sequence: 1 ctgcaggaattcsmycgcat.....gctcccaacgcgttggaggt 2692

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_NA:*
1:    /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:    /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
25:   /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26:   /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2690.8	100.0	2692	9	US-09-908-322-11	Sequence 11, Appl
2	2690.8	100.0	2692	10	US-09-783-931-11	Sequence 11, Appl
3	2666.2	99.0	2692	20	US-10-877-563-13	Sequence 13, Appl
4	2577.8	95.8	2857	19	US-10-731-741-9	Sequence 9, Appli
5	2577.8	95.8	2857	21	US-10-764-420-2345	Sequence 2345, Ap
6	2506.6	93.1	2857	9	US-09-908-322-4	Sequence 4, Appli
7	2506.6	93.1	2857	10	US-09-783-931-4	Sequence 4, Appli
8	2133.4	79.2	2899	9	US-09-908-322-	

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:13:45 ; Search time 10555.3 Seconds
(without alignments)
10411.464 Million cell updates/sec

Title: US-09-783-931A-11
Perfect score: 2692
Sequence: 1 ctgcaggaattctsmycgcat.....gctcccaacgcgttgaggt 2692

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
1: /cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq:*
3: /.seq:*
129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2690.8	100.0	2692	34	US-09-783-931-11	Sequence 11, Appl
2	2666.2	99.0	2692	20	US-09-310-685-13	Sequence 13, Appl
3	2666.2	99.0	2692	64	US-10-877-563-13	Sequence 13, Appl
4	2666.2	99.0	2692	68	US-11-022-478-13	Sequence 13, Appl
5	2582.6	95.9	2857	48	US-10-144-771-1551	Sequence 1551, Ap
6	2582.6	95.9	2857	106	US-60-360-207-1551	Sequence 1551, Ap
7	2577.8	95.8	2857	62	US-10-731-741-9	Sequence 9, Appli
8	2577.8	95.8	2857	62	US-10-764-420-2345	Sequence 2345, Ap
9	2506.6	93.1	2857	34	US-09-783-931-4	Sequence 4, Appli
10	2436.8	90.5	2988	65	US-10-913-487-12	Sequence 12, Appl
11	2133.4	79.2	2899	34	US-09-783-931-24	Sequence 24, Appl
12	2123.8	78.9	2795	2	PCT-US03-03482-3930	Sequence 3930, Ap
13	2123.8	78.9	2795	53	US-10-357-507-3930	Sequence 3930, Ap
14	1982.8	73.7	2926	65	US-10-913-487-13	Sequence 13, Appl

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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 70.7929 Seconds
(without alignments)
761.328 Million cell updates/sec

Title: US-09-783-931A-12
Perfect score: 4121
Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	4121	100.0	722	3	US-08-981-392-12	Sequence 12, Appl	
2	4121	100.0	722	4	US-09-908-322-12	Sequence 12, Appl	
3	3971	96.4	720	3	US-08-872-855-4	Sequence 4, Appli	
4	3840.5	93.2	713	3	US-08-872-855-5	Sequence 5, Appli	
5	3659.5	88.8	723	3	US-09-068-740A-9	Sequence 9, Appli	
6	3659.5	88.8	723	4	US-09-423-753-27	Sequence 27, Appl	
7	3631.5	88.1	723	4	US-09-641-612-6	Sequence 6, Appli	
8	3571.5	86.7	702	3	US-09-068-740A-4	Sequence 4, Appli	
9	3368	81.7	728	3	US-08-981-392-2	Sequence 2, Appli	
10	3368	81.7	728	4	US-09-908-322-2	Sequence 2, Appli	
11							

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OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 247.116 Seconds
(without alignments)
1130.390 Million cell updates/sec

Title: US-09-783-931A-12
Perfect score: 4121
Sequence: 1 MGRRSALALAVVSALLCQVW.....YQSVYVLSAEKDECVIATEV 722

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	4121	100.0	722	9	US-09-908-322-12	Sequence 12, Appl	
2	4121	100.0	722	10	US-09-783-931-12	Sequence 12, Appl	
3	4007	97.2	722	16	US-10-877-563-14	Sequence 14, Appl	
4	4003	97.1	722	15	US-10-042-865-107	Sequence 107, App	
5	4003	97.1	722	16	US-10-731-741-4	Sequence 4, Appli	
6	3971	96.4	720	14	US-10-417-719-4	Sequence 4, Appli	
7	3848	93.4	714	15	US-10-042-865-108	Sequence 108, App	
8	3840.5	93.2	713	14	US-10-417-719-5	Sequence 5, Appli	
9	3659.5	88.8	723	9	US-09-828-366-21	Sequence 21, Appl	
10	3659.5	88.8	723	9	US-09-995-593A-9	Sequence 9, Appli	
11	3659.5	88.8	723	14	US-10-028-072-346	Sequence 346, App	

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 85.8422 Seconds
(without alignments)
10007.261 Million cell updates/sec

Title: US-09-783-931A-14
Perfect score: 525
Sequence: 1 tacgatgaayaacctggcga.....aggacgagtgcgatcatcgca 525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	521.4	99.3	525	3	US-08-981-392-14	Sequence 14, Appl	
2	521.4	99.3	525	4	US-09-908-322-14	Sequence 14, Appl	
3	188.6	35.9	2183	4	US-09-641-612-9	Sequence 9, Appli	
4	188.6	35.9	2663	3	US-09-068-740A-8	Sequence 8, Appli	
5	188.6	35.9	2663	4	US-09-423-753-8	Sequence 8, Appli	
6	174.8	33.3	1981	3	US-08-981-392-26	Sequence 26, Appl	
7	174.8	33.3	1981	4	US-09-908-322-26	Sequence 26, Appl	
8	159.6	30.4	2899	3	US-08-981-392-24	Sequence 24, Appl	
9	159.6	30.4	2899	4	US-09-908-322-24		

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 323.543 Seconds
(without alignments)
10210.150 Million cell updates/sec

Title: US-09-783-931A-14
Perfect score: 525
Sequence: 1 tacgatgaayaacctggcga.....aggacgagtgcgatcatcgca 525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	IDB	ID	Description
1	521.4	99.3	525	9	US-09-908-322-14	Sequence 14, Appl
2	521.4	99.3	525	10	US-09-783-931-14	Sequence 14, Appl
3	519.4	98.9	525	20	US-10-877-563-15	Sequence 15, Appl
4	282.4	53.8	468	10	US-09-918-995-29101	Sequence 29101, A
5	188.6	35.9	2183	19	US-10-644-548-9	Sequence 9, Appli
6	188.6	35.9	2663	9	US-09-995-593A-8	Sequence 8, Appli
7	188.6	35.9	2663	14	US-10-241-476-8	Sequence 8, Appli
8	188.6	35.9	2663	24	US-11-051-618B-8	Sequence 8, Appli
9	188.6	35.9	2663	24	US-11-051-631-8	Sequence 8, Appli
10	188.6	35.9	2933	9	US-09-828-366-20	Sequence 20, Appl
11	188.6	35.9	2933	14	US-10-028-072-345	

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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 71.3812 Seconds
(without alignments)
761.328 Million cell updates/sec

Title: US-09-783-931A-2
Perfect score: 4153
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIATEV 728

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	4153	100.0	728	3	US-08-981-392-2	Sequence 2, Appli	
2	4153	100.0	728	4	US-09-908-322-2	Sequence 2, Appli	
3	4142.5	99.7	729	3	US-08-872-855-8	Sequence 8, Appli	
4	3495.5	84.2	721	3	US-08-981-392-5	Sequence 5, Appli	
5	3495.5	84.2	721	4	US-09-908-322-5	Sequence 5, Appli	
6	3494.5	84.1	723	3	US-09-068-740A-9	Sequence 9, Appli	
7	3494.5	84.1	723	4	US-09-423-753-27	Sequence 27, Appli	
8	3491.5	84.1	721	3	US-08-872-855-7	Sequence 7, Appli	
9	3466.5	83.5	723	4	US-09-641-612-6		

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OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 249.169 Seconds
(without alignments)
1130.390 Million cell updates/sec

Title: US-09-783-931A-2
Perfect score: 4153
Sequence: 1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIATEV 728

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4153	100.0	728	9 US-09-908-322-2	Sequence 2, Appli
2	4153	100.0	728	10 US-09-783-931-2	Sequence 2, Appli
3	4142.5	99.7	729	14 US-10-417-719-8	Sequence 8, Appli
4	4135	99.6	728	16 US-10-877-563-11	Sequence 11, Appl
5	3495.5	84.2	721	9 US-09-908-322-5	Sequence 5, Appli
6	3495.5	84.2	721	10 US-09-783-931-5	Sequence 5, Appli
7	3495.5	84.2	721	15 US-10-042-865-109	Sequence 109, App
8	3494.5	84.1	723	9 US-09-828-366-21	Sequence 21, Appl
9	3494.5	84.1	723	9 US-09-995-593A-9	Sequence 9, Appli

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 13:02:24 ; Search time 323.911 Seconds
(without alignments)
10007.261 Million cell updates/sec

Title: US-09-783-931A-26
Perfect score: 1981
Sequence: 1 cattgggtacgggccccct.....attccgntttcaaagttttt 1981

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1956	98.7	1981	3	US-08-981-392-26	Sequence 26, Appl
2	1956	98.7	1981	4	US-09-908-322-26	Sequence 26, Appl
3	1780	89.9	2899	3	US-08-981-392-24	Sequence 24, Appl
4	1780	89.9	2899	4	US-09-908-322-24	Sequence 24, Appl
5	1526.2	77.0	2663	3	US-09-068-740A-8	Sequence 8, Appli
6	1526.2	77.0	2663	4	US-09-423-753-8	Sequence 8, Appli
7	1524.6	77.0	2183	4	US-09-641-612-9	Sequence 9, Appli
8	1134.2	57.3	2692	3	US-08-981-392-11	Sequence 11, Appl
9	1134.2	57.3	2692	4	US-09-908-	

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: July 14, 2005, 18:14:14 ; Search time 1220.84 Seconds
(without alignments)
10210.150 Million cell updates/sec

Title: US-09-783-931A-26
Perfect score: 1981
Sequence: 1 cattgggtacgggccccct.....attccgntttcaaagttttt 1981

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6340675 seqs, 3146120178 residues

Total number of hits satisfying chosen parameters: 12681350

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1956	98.7	1981	9	US-09-908-322-26	Sequence 26, Appl	
2	1956	98.7	1981	10	US-09-783-931-26	Sequence 26, Appl	
3	1943.8	98.1	1981	20	US-10-877-563-16	Sequence 16, Appl	
4	1780	89.9	2899	9	US-09-908-322-24	Sequence 24, Appl	
5	1780	89.9	2899	10	US-09-783-931-24	Sequence 24, Appl	
6	1526.2	77.0	2663	9	US-09-995-593A-8	Sequence 8, Appli	
7	1526.2	77.0	2663	14	US-10-241-476-8	Sequence 8, Appli	
8	1526.2	77.0	2663	24	US-11-051-618B-8	Sequence 8, Appli	
9	1526.2	77.0	2663	24	US-11-051-631-8	Sequence 8, Appli	
10	1526.2	77.0	2933	9	US-09-828-366-20	Sequence 20, Appl	
11	1526.2	77.0	2933	14	US-10-028-072-345	Sequence	

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OM protein - protein search, using sw model

Run on: July 14, 2005, 19:09:59 ; Search time 18.8258 Seconds
(without alignments)
761.328 Million cell updates/sec

Title: US-09-783-931A-65
Perfect score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP.....CNQDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1160	100.0	192	3	US-08-981-392-65	Sequence 65, Appl	
2	1160	100.0	192	4	US-09-908-322-65	Sequence 65, Appl	
3	1160	100.0	276	3	US-08-981-392-43	Sequence 43, Appl	
4	1160	100.0	276	4	US-09-908-322-43	Sequence 43, Appl	
5	1160	100.0	520	3	US-09-068-740A-3	Sequence 3, Appli	
6	1160	100.0	702	3	US-09-068-740A-4	Sequence 4, Appli	
7	1160	100.0	723	3	US-09-068-740A-9	Sequence 9, Appli	
8	1160	100.0	723	4	US-09-423-753-27	Sequence 27, Appl	
9	1153	99.4	723	4	US-09-641-612-6	Sequence 6, Appli	
10	1138	98.1	728	3	US-08-981-392-2	Sequence 2, Appli	
11	1138	98.1	728	4	US-09-908-322-2		

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OM protein - protein search, using sw model

Run on: July 15, 2005, 03:54:30 ; Search time 65.715 Seconds
(without alignments)
1130.390 Million cell updates/sec

Title: US-09-783-931A-65
Perfect score: 1160
Sequence: 1 GFTWPGTFSLIIEALHTDSP.....CNQDLNYCTHHKPKNGATC 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3:
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1160	100.0	192	9	US-09-908-322-65	Sequence 65, Appl	
2	1160	100.0	192	10	US-09-783-931-65	Sequence 65, Appl	
3	1160	100.0	192	16	US-10-877-563-17	Sequence 17, Appl	
4	1160	100.0	276	9	US-09-908-322-43	Sequence 43, Appl	
5	1160	100.0	276	10	US-09-783-931-43	Sequence 43, Appl	
6	1160	100.0	331	17	US-10-846-989-24	Sequence 24, Appl	
7	1160	100.0	331	18	US-10-845-834A-24	Sequence 24, Appl	
8	1160	100.0	369	17	US-10-846-989-29	Sequence 29, Appl	
9	1160	100.0	369	18	US-10-845-834A-29	Sequence 29, Appl	
10	1160	100.0	484	17	US-10-846-989-34	Sequence 34, Appl	
11	1160	100.0	484	18	US-10-845-834A-34	Sequence 34, Appl	
12	1160	100.0	520	9	US-09-995-593A-3	Sequence 3, Appli	

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:49:23 ; Search time 165 Seconds
(without alignments)
410.200 Million cell updates/sec

Title: US-09-783-931A-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	908	98.1	175	2	AAW11724	Aaw11724	H-Delta-1
2	678.5	73.3	175	2	AAW11721	Aaw11721	H-Delta-1
3	527.5	57.0	702	2	AAW18349	Aaw18349	Prolifera
4	527.5	57.0	702	2	AAW75495	Aaw75495	Truncated
5	527.5	57.0	723	2	AAW18353	Aaw18353	Prolifera
6	527.5	57.0	723	2	AAW75492	Aaw75492	Human del
7	527.5	57.0	723	2	AAW94498	Aaw94498	Human del
8	527.5	57.0	723	3	AAW83227	Aay83227	PRO172 Po
9	527.5	57.0	723	3	AAB33422		

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:53:29 ; Search time 42 Seconds
(without alignments)
311.038 Million cell updates/sec

Title: US-09-783-931A-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	916	98.9	175	3	US-08-981-392-23	Sequence 23, Appl	
2	916	98.9	175	4	US-09-908-322-23	Sequence 23, Appl	
3	631.5	68.2	118	3	US-08-981-392-17	Sequence 17, Appl	
4	631.5	68.2	118	4	US-09-908-322-17	Sequence 17, Appl	
5	527.5	57.0	702	3	US-09-068-740A-4	Sequence 4, Appli	
6	527.5	57.0	723	3	US-09-068-740A-9	Sequence 9, Appli	
7	527.5	57.0	723	4	US-09-423-753-27	Sequence 27, Appl	
8	527.5	57.0	723	4	US-09-641-612-6	Sequence 6, Appli	
9	448	48.4	713	3	US-08-872-855-5	Sequence 5, Appli	
10	428	46.2	720	3	US-08-872-855-4	Sequence 4, Appli	
11	419	45.2	722	3	US-08-981-392-12	Sequence 12, Appl	

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:56:20 ; Search time 164 Seconds
(without alignments)
412.844 Million cell updates/sec

Title: US-09-783-931A-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1729182 seqs, 386893608 residues

Total number of hits satisfying chosen parameters: 1729182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	916	98.9	175	9 US-09-908-322-23	Sequence 23, Appl
2	916	98.9	175	10 US-09-783-931-23	Sequence 23, Appl
3	631.5	68.2	118	9 US-09-908-322-17	Sequence 17, Appl
4	631.5	68.2	118	10 US-09-783-931-17	Sequence 17, Appl
5	527.5	57.0	702	9 US-09-995-593A-4	Sequence 4, Appli
6	527.5	57.0	702	20 US-11-051-631-4	Sequence 4, Appli
7	527.5	57.0	723	9 US-09-828-366-21	Sequence 21, Appl
8	527.5	57.0	723	9 US-09-995-593A-9	Sequence 9, Appli

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:50:15 ; Search time 40 Seconds
(without alignments)
420.948 Million cell updates/sec

Title: US-09-783-931A-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428	46.2	722	2	I48324	DELTA-like 1 - mou
2	388	41.9	728	2	I50719	C-Delta-1 - chicke
3	126.5	13.7	685	2	JC7570	Delta-4 protein -
4	125.5	13.6	686	2	JC7569	Delta-4 protein -
5	88.5	9.6	1106	1	TVHUGL	transforming prote
6	87.5	9.4	925	2	T29311	hypothetical prote
7	86.5	9.3	504	2	T13475	hypothetical prote
8	83.5	9.0	1651	2	T14160	transmembrane rece
9	83	9.0	1707	2	T18951	hypothetical prote
10	81	8.7	763	2	AC0108	probable primase Y
11	79.5	8.6	326	2	A41732	heterogeneous ribo
12	79.5	8.6	386	1	S22315	snRNP-associated p
13	78.5	8.5	512	2	T47793	receptor-like prot
14	77.5	8.4	538	2	T49418	hypothetical prote

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OM protein - protein search, using sw model

Run on: July 15, 2005, 14:50:15 ; Search time 175 Seconds
(without alignments)
512.079 Million cell updates/sec

Title: US-09-783-931A-23
Perfect score: 926
Sequence: 1 TMNNLANCQREKDISVSIIG.....DTKYQSVYVISEEKDECVIA 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	527.5	57.0	723	1 DLL1_HUMAN	O00548 homo sapien
2	445	48.1	714	1 DLL1_RAT	P97677 rattus norv
3	431	46.5	722	2 Q6PFV7	Q6pfv7 mus musculu
4	428	46.2	722	1 DLL1_MOUSE	Q61483 mus musculu
5	388	41.9	728	2 Q90656	Q90656 gallus gall
6	387.5	41.8	726	2 Q8AW87	Q8aw87 cynops pyrr
7	356	38.4	721	2 Q91902	Q91902 xenopus lae
8	294.5	31.8	717	2 P87357	P87357 brachydanio
9	294.5	31.8	720	2 Q8UWJ4	Q8uwj4 brachydanio
10	218	23.5	772	2 Q6DI48	Q6di48 brachydanio
11	149	16.1	802	2 O57462	O57462 brachydanio
12	126.5	13.7	685	1 DLL4_HUMAN	Q9nr61 homo sapien
13	126.5	13.7	686	1 DLL4_MOUSE	Q9ji71 mus musculu
14	125.5	13.6	686	2 Q9DBU9	Q9dbu9 mus musculu
15	91	9.8	364	2 Q6MZM8	Q6mzm8 homo sapien